

**AMENDMENTS TO THE SPECIFICATION**

**Please replace the paragraph at page 13, line 10, to page 14, line 9 with the following amended paragraph:**

Herein, an input region of a hybrid-sensor kinase is a region present at the N-terminal of the kinase, and have a transmembrane region in many cases. The transmembrane region can be revealed by a structure prediction analysis using a structure prediction software, for example, TMpred program [K. Hofmann & W. Stoffel, Biol. Chem. Hoppe-Seyler, 374, 166 (1993)] which is available, for example, from [http://www.ch.embnet.org/software/TMPRED\\_form.html](http://www.ch.embnet.org/software/TMPRED_form.html) ~~http://www.ch.embnet.org/software/TMPRED\_form.html~~ [www.ch.embnet.org/software/TMPRED\\_form.html](http://www.ch.embnet.org/software/TMPRED_form.html). A histidine kinase region of a hybrid-sensor kinase is, for example, a region following the C-terminal of the input region, and is a region characterized in that it has five conserved motifs common to general histidine kinases as described in Parkinson, J.S. & Kofoed, E.C. (1989) Annual Review of Genetics 23:311-336, Stock, J.B. et. al. (1989) Microbiological Reviews 53(4):450-490. For example, in the hybrid-sensor kinase SLN1 of budding yeast, a histidine kinase region is the region from amino acid residues 556 to 908. A receiver region of a hybrid-sensor kinase is, for example, a region following the C-terminal of the histidine kinase region, and is a region characterized in that it has three conserved motifs common to general histidine kinases as described in Parkinson, J.S. & Kofoed, E.C. Annual Review of Genetics 23:311-336(1989), Stock, J.B. et. al.(1989) Microbiological Reviews 53(4): 450-490. For example, in the hybrid-sensor kinase SLN1 of budding yeast, a receiver region is the region from amino acid residues 1088 to 1197.

**Please replace the paragraph at page 24, line 21, to page 25, line 18 with the following amended paragraph:**

In the present invention, “homology” refers to identity of sequences between two genes or two proteins. The “homology” is determined by comparing two sequences aligned in the optimal state, over a region of a sequence of a subject to be compared. Herein, in optimal alignment of nucleotide sequences or amino acid sequences to be compared, addition or deletion (e.g. gap etc.) may be allowable. Such the “homology” can be calculated by homology analysis with making alignment using a program of FASTA [Pearson & Lipman, Proc. Natl. Acad. Sci. USA, 4, 2444-2448(1998)], BLAST [Altschul et. al. Journal of Molecular Biology, 215, 403-410(1990)], CLUSTAL W [Thompson, Higgins & Gibson, Nucleic Acid Research, 22, 4673-4680(1994a)] and the like. The above programs are available to the public, for example, in homepage (~~http://www.ddbj-nig.ac.jp~~) ([www.ddbj.nig.ac.jp](http://www.ddbj.nig.ac.jp)) of DNA Data Bank of Japan [international DNA Data Bank managed in Center for Information Biology and DNA Data Bank of Japan (CIB/DDBJ)]. Alternatively, the “homology” may be also obtained by using commercially available sequence analysis software. Specifically, the homology can be calculated, for example, by performing homology analysis with making alignment by the Lipman-Pearson method [Lipman, D. J. and Pearson, W. R., Science, 227, 1435-1441,(1985)] using GENETYX-WIN Ver.5 (manufactured by Software Development Co., Ltd.).

**Please replace the paragraph at page 33, lines 3 to 16 with the following amended paragraph:**

Example of the “osmosensing histidine kinase having no transmembrane region” include HIK1 of *Magnaporthe grisea*. The *hik1* gene is a gene homologous to *Neurospora crassa* *os-1* gene, and a nucleotide sequence and an amino acid sequence are published (nucleotide sequence: Genebank accession AB041647, amino acid sequence: GeneBank accession BAB40947). It is known that HIK1 has the aforementioned structural characteristics such as lack of the transmembrane region based on its amino acid sequence. In addition, it is observed that *Magnaporthe grisea* deficient in the *hik1* gene has the higher osmolarity sensitivity than that of a wild strain, demonstrating that HIK1 is an osmosensing histidine kinase ([http://www.sci.saitama-u.ac.jp/seitai/iden/Japanese/Abst\\_Symp3.html](http://www.sci.saitama-u.ac.jp/seitai/iden/Japanese/Abst_Symp3.html)) ([www.sci.saitama-u.ac.jp/seitai/iden/Japanese/Abst\\_Symp3.html](http://www.sci.saitama-u.ac.jp/seitai/iden/Japanese/Abst_Symp3.html)).